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MASRCH (TM)

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Release 2.1D John F. Collins, Biocomputing Research Unit.  
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jan 21 18:50:59 1997; MasPar time 11.31 Seconds  
639.201 Million cell updates/sec

Tabular output not generated.

Title: >US-08-469-637-2  
Description: (1-390) from US08469637.pep (1 of 2)  
Perfect Score: 2927  
Sequence: 1 MNKLLCCALVFLDISIKWTT.....VPSQLHNVQIVSEVIFRNDR 390

Scoring table: PAM 150  
Gap 11

Searched: 52205 seqs, 18531385 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot33  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10

Statistics: Mean 47.266; Variance 77.924; scale 0.607

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	No.	Score	% Match	Query Length	DB	ID	Description	Pred. No.
1	405	13.8	461	9	TNR2_HUMAN	TUMOR NECROSIS FACTOR	1.65e-65	
2	375	12.8	474	9	TNR2_MOUSE	TUMOR NECROSIS FACTOR	1.58e-58	
3	303	10.4	277	2	CD40_HUMAN	CD40L RECEPTOR PRECUR	4.15e-42	
4	294	10.0	305	2	CD40_MOUSE	CD40L RECEPTOR PRECUR	4.26e-40	

5	269	9.2	326	9	VT2_MYXVL	TUMOR NECROSIS FACTOR	1.43e-34
6	260	8.9	325	9	VT2_SFVKA	TUMOR NECROSIS FACTOR	1.32e-32
7	260	8.9	435	9	TNRL_HUMAN	LYMPHOTOXIN-BETA RECE	1.32e-32
8	233	8.0	349	9	VC22_VARV	PROTEIN C22/B28 HOMOL	8.41e-27
9	221	7.6	454	9	TNR1_MOUSE	TUMOR NECROSIS FACTOR	2.86e-24
10	220	7.5	461	9	TNR1_RAT	TUMOR NECROSIS FACTOR	4.63e-24
11	215	7.3	416	6	NGFR_CHICK	LOW-AFFINITY NERVE GR	5.12e-23
12	213	7.3	427	6	NGFR_HUMAN	LOW-AFFINITY NERVE GR	1.33e-22
13	207	7.1	425	6	NGFR_RAT	LOW-AFFINITY NERVE GR	2.32e-21
14	178	6.1	595	2	CD30_HUMAN	CD30L RECEPTOR PRECUR	1.62e-15
15	172	5.9	455	9	TNR1_HUMAN	TUMOR NECROSIS FACTOR	2.42e-14
16	159	5.4	256	1	41BB_MOUSE	4-1BB LIGAND RECEPTOR	7.53e-12
17	159	5.4	260	2	CD27_HUMAN	CD27L RECEPTOR PRECUR	7.53e-12
18	146	5.0	271	6	OX40_RAT	OX40L RECEPTOR PRECUR	1.96e-09
19	144	4.9	272	6	OX40_MOUSE	OX40L RECEPTOR PRECUR	4.52e-09
20	140	4.8	255	1	41BB_HUMAN	4-1BB LIGAND RECEPTOR	2.38e-08
21	141	4.8	277	6	OX40_HUMAN	OX40L RECEPTOR PRECUR	1.57e-08
22	137	4.7	327	3	FASA_MOUSE	FASL RECEPTOR PRECURS	8.14e-08
23	134	4.6	250	2	CD27_MOUSE	CD27L RECEPTOR PRECUR	2.75e-07
24	134	4.6	335	3	FASA_HUMAN	FASL RECEPTOR PRECURS	2.75e-07
25	124	4.2	103	9	VA53_VACCV	PROTEIN A53.	1.44e-05
26	124	4.2	103	9	VA53_VACCC	PROTEIN A53.	1.44e-05
27	115	3.9	360	10	YIH9_YEAST	HYPOTHETICAL 41.6 KD	4.40e-04
28	105	3.6	2813	9	VWF_HUMAN	VON WILLEBRAND FACTOR	1.62e-02
29	102	3.5	3084	5	LMA1_MOUSE	LAMININ ALPHA-1 CHAIN	4.59e-02
30	100	3.4	1752	3	DESP_HUMAN	DESMOPLAKIN I AND II	9.05e-02
31	96	3.3	1104	8	SYV_YEAST	VALYL-TRNA SYNTHETASE	3.42e-01
32	96	3.3	1356	5	KAB7_YEAST	PROBABLE SERINE/THREO	3.42e-01
33	98	3.3	1947	6	MYSC_CAEEL	MYOSIN HEAVY CHAIN C	1.77e-01
34	96	3.3	2767	9	THYG_HUMAN	THYROGLOBULIN PRECURS	3.42e-01
35	96	3.3	3707	6	PGBM_MOUSE	BASEMENT MEMBRANE-SPE	3.42e-01
36	97	3.3	4092	3	DYHC_YEAST	DYNEIN HEAVY CHAIN, C	2.46e-01
37	94	3.2	122	9	VC22_VACCC	PROTEIN C22/B28.	6.54e-01
38	95	3.2	125	9	TNPF_STA AU	TRANSPOSASE FOR TRANS	4.73e-01
39	93	3.2	218	5	MERB_BACSR	ALKYLMERCURY LYASE (E	9.00e-01
40	95	3.2	916	8	RTJK_DROME	RNA-DIRECTED DNA POLY	4.73e-01
41	93	3.2	1122	9	TIE2_MOUSE	TYROSINE-PROTEIN KINA	9.00e-01
42	93	3.2	1429	5	LI12_CAEEL	LIN-12 PROTEIN PRECUR	9.00e-01
43	94	3.2	1609	5	LMG1_HUMAN	LAMININ GAMMA-1 CHAIN	6.54e-01
44	94	3.2	1966	6	MYSB_CAEEL	MYOSIN HEAVY CHAIN B	6.54e-01
45	95	3.2	2769	9	THYG_BOVIN	THYROGLOBULIN PRECURS	4.73e-01

# ALIGNMENTS

RESULT 1

ID TNR2\_HUMAN STANDARD; PRT; 461 AA.

AC P20333;

DT 01-FEB-1991 (REL. 17, CREATED)

DT 01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)

DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)

DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR

DE BINDING PROTEIN 2) (TBPII) (P80) (TNF-R2) (P75) (CD120B).

GN TNFR2 OR TNFR.

OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 90260639.  
 RA SMITH C.A., DAVIS T., ANDERSON D., SOLAM L., BECKMANN M.P., JERZY R.,  
 RA DOWER S.K., COSMAN D., GOODWIN R.G.;  
 RL SCIENCE 248:1019-1023(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 91045991.  
 RA KOHNO T., BREWER M.T., BAKER S.L., SCHWARTZ P.E., KING M.W.,  
 RA HALE K.K., SQUIRES C.H., THOMPSON R.C., VANNICE J.L.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 87:8331-8335(1990).  
 RN [3]  
 RP SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE; 90349572.  
 RA HELLER R.A., SONG K., ONASCH M.A., FISCHER W.H., CHANG D.,  
 RA RINGOLD G.M.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 87:6151-6155(1990).  
 RN [4]  
 RP SEQUENCE OF 27-31.  
 RX MEDLINE; 90110215.  
 RA ENGELMANN H., NOVICK D., WALLACH D.;  
 RL J. BIOL. CHEM. 265:1531-1536(1990).  
 RN [5]  
 RP SEQUENCE OF 22-40; 65-69; 136-141; 300-306 AND 346-362.  
 RX MEDLINE; 91056048.  
 RA LOETSCHER H., SCHLAEGER E.J., LAHM H.-W., PAN Y.-C.E., LESSLAUER W.,  
 RA BROCKHAUS M.;  
 RL J. BIOL. CHEM. 265:20131-20138(1990).  
 RN [6]  
 RP CHARACTERIZATION.  
 RX MEDLINE; 93016040.  
 RA PENNICA D., LAM V.T., MIZE N.K., WEBER R.F., LEWIS M., FENDLY B.M.,  
 RA LIPARI M.T., GOEDEL D.V.;  
 RL J. BIOL. CHEM. 267:21172-21178(1992).  
 CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNA-ALPHA AND  
 CC APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.  
 CC -!- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW  
 CC LEVEL ON THREONINE RESIDUES.  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL; M32315; G189186; -.  
 DR EMBL; M35857; G339752; -.  
 DR EMBL; M55994; G339758; -.  
 DR PIR; A35356; A35356.  
 DR PIR; A36007; A36007.  
 DR PIR; A36475; A36475.  
 DR PIR; B35010; B35010.  
 DR PIR; A23666; A23666.  
 DR HSSP; P19438; 1TNR.  
 DR MIM; 191191; 11TH EDITION.



GN TNFR-2.  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 91187885.  
 RA LEWIS M., TARTAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.,  
 RA WONG G.H., CHEN E.Y., GOEDDEL D.V.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 88:2830-2834 (1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 91246168.  
 RA GOODWIN R.G., ANDERSON D., JERZY R., DAVIS T., BRANNAN C.I.,  
 RA COPELAND N.G., JENKINS N.A., SMITH C.A.;  
 RL MOL. CELL. BIOL. 11:3020-3026 (1991).  
 CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA.  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL; M60469; G199828; -.  
 DR EMBL; M59378; G202095; -.  
 DR PIR; B38634; B38634.  
 DR HSSP; P19438; 1TNR.  
 DR PROSITE; PS00652; TNFR\_NGFR.  
 KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.  
 FT SIGNAL 1 22  
 FT CHAIN 23 474 TUMOR NECROSIS FACTOR RECEPTOR 2.  
 FT DOMAIN 23 258 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 259 288 POTENTIAL.  
 FT DOMAIN 289 474 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 39 203 4 X TNFR-CYS.  
 FT REPEAT 39 77 TNFR-CYS 1.  
 FT REPEAT 78 119 TNFR-CYS 2.  
 FT REPEAT 120 164 TNFR-CYS 3.  
 FT REPEAT 165 203 TNFR-CYS 4.  
 FT DISULFID 40 54 BY SIMILARITY.  
 FT DISULFID 55 68 BY SIMILARITY.  
 FT DISULFID 58 76 BY SIMILARITY.  
 FT DISULFID 79 94 BY SIMILARITY.  
 FT DISULFID 97 111 BY SIMILARITY.  
 FT DISULFID 101 119 BY SIMILARITY.  
 FT DISULFID 121 127 BY SIMILARITY.  
 FT DISULFID 136 145 BY SIMILARITY.  
 FT DISULFID 139 163 BY SIMILARITY.  
 FT DISULFID 166 181 BY SIMILARITY.  
 FT CARBOHYD 69 69 POTENTIAL.  
 FT CARBOHYD 195 195 POTENTIAL.  
 SQ SEQUENCE 474 AA; 50319 MW; DC32B2B6 CRC32;

Query Match 12.8%; Score 375; DB 9; Length 474;  
 Best Local Similarity 41.5%; Pred. No. 1.58e-58;  
 Matches 66; Conservative 21; Mismatches 61; Indels 11; Gaps 7;

Db 52 qmccakcpgpggyvkhfcnktsdtvcadceasmvtqvwngfrtclscsssccttdqveirac 111

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Qy    38 QLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECLYCSPVCKELQYVKQEC 97

Db    112 tkqqrncvaceagrycalkthsgscrqcmrlskcpgpgfgvassrapngnvlckacapgtf 171
      : : | | | | | | | | | | | | | | : : | : | : | : |
Qy    98 NRTHNRVCECKEGRY--LEIEF--CLKH-R-S-CPPGFGVVQAGTPERN TVCKRCPDGFF 150

Db    172 sdttsstdvcrphricsi--laip--gnastdavcapes 206
      | : | | | | | | | | : | : | | | : | : | : |
Qy    151 SNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNS 189

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RESULT 3

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ID    CD40_HUMAN      STANDARD;      PRT;      277 AA.
AC    P25942;
DT    01-MAY-1992 (REL. 22, CREATED)
DT    01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT    01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE    CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).
GN    CD40.
OS    HOMO SAPIENS (HUMAN).
OC    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC    EUTHERIA; PRIMATES.
RN    [1]
RP    SEQUENCE FROM N.A.
RX    MEDLINE; 89356608.
RA    STAMENKOVIC I., CLARK E.A., SEED B.;
RL    EMBO J. 8:1403-1410(1989).
CC    -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC    -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC    -!- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.
CC    -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR    EMBL; X60592; G29851; -.
DR    PIR; S04460; S04460.
DR    MIM; 109535; 11TH EDITION.
DR    PROSITE; PS00652; TNFR_NGFR.
KW    RECEPTOR; B-CELL; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.
FT    SIGNAL          1      19      POTENTIAL.
FT    CHAIN           20     277     CD40L RECEPTOR.
FT    DOMAIN          20     193     EXTRACELLULAR (POTENTIAL).
FT    TRANSMEM        194     215     POTENTIAL.
FT    DOMAIN          216     277     CYTOPLASMIC (POTENTIAL).
FT    DOMAIN          25     187     4 X TNFR-CYS.
FT    REPEAT          25      60     TNFR-CYS 1.
FT    REPEAT          61     103     TNFR-CYS 2.
FT    REPEAT          104     144     TNFR-CYS 3.
FT    REPEAT          145     187     TNFR-CYS 4.
FT    CARBOHYD        153     153     POTENTIAL.
FT    CARBOHYD        180     180     POTENTIAL.
SQ    SEQUENCE      277 AA;  30619 MW;  3B284411 CRC32;

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Query Match          10.4%;  Score 303;  DB 2;  Length 277;
Best Local Similarity 36.8%;  Pred. No. 4.15e-42;
Matches      56;  Conservative 21;  Mismatches 67;  Indels 8;  Gaps 7;

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Db	38	cslcqpggklvsdcteftetecclpcgesefldtnwrethchghkycdpn-lglr-vqgkg	95
		: : :         :	
Qy	41	CDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDEC-L--YCSPVCKELQYVKQEC	97
Db	96	tsetdtictceegwhctseacescvlhrscspgfgvkqiatgvsdticepcpvgffsnvs	155
		: :       :     :       :         :   : :         :	
Qy	98	NRTHNRVCECKEGRY-L-EI-EFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNET	154
Db	156	safekchpwtscetkdlvvqgagtnktdvvcg	187
		:   :   :   :       :   :	
Qy	155	SSKAPCRKHTNCSVFGLLLTQKGNATHDNICS	186

Query Match 10.0%; Score 294; DB 2; Length 305;  
Best Local Similarity 38.8%; Pred. No. 4.26e-40;  
Matches 59; Conservative 20; Mismatches 65; Indels 8; Gaps 6;

Db 38 cdlcqpgsrltshctalektqchpcdsgefsaqwnreirchqhrhcepn-qggr-vkkeg 95  
 || | ||: | ||| || | || :: |: | | | : || |  
 Qy 41 CDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDEC-LY--CSPVCKELQYVKQEC 97  
  
 Db 96 taesdtvctckegqhctskdceacaqhtpcipgfgvmematettdtvchpcpvvgffsnqs 155  
 : || |||: : | | | : | ||||:: : | : || | || ||||:::  
 Qy 98 NRTHNRVCECKEGRY-L--EIEFCLKHRSCPPGFGVVQAGTPERN TVCKRCPDGFFSNET 154  
  
 Db 156 slfekcypwtscedknlevlqkgtsqtnvicg 187  
 | | | : | : ||| : : ||:  
 Qy 155 SSKAPCRKHTNCSVFGLLLTQKGNATHDNICS 186